

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/570,121
Source: JFWP
Date Processed by STIC: 11/17/2006

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 11/17/2006

PATENT APPLICATION: US/10/570,121

TIME: 08:38:11

Input Set : F:\ARS-125-SEQ LIST.txt

Output Set: N:\CRF4\11172006\J570121.raw

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3 <110> APPLICANT: APPLIED RESEARCH SYSTEMS ARS HOLDING N.V.
5 <120> TITLE OF INVENTION: NOVEL UBP8rp POLYPEPTIDES AND THEIR USE IN THE TREATMENT OF
PSORIASIS
7 <130> FILE REFERENCE: WO 886
C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/570,121
C--> 9 <141> CURRENT FILING DATE: 2006-02-28
9 <160> NUMBER OF SEQ ID NOS: 79
11 <170> SOFTWARE: PatentIn version 3.1
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15 <212> TYPE: DNA
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51 gtttctgtgt ctccagttga tagacatgtg gattcctcca gttagggttt gttattaatg 180
53 aagccactat aaataactgc ttacaagtgt ggacttacat ttttatttct tttggataaa 240
55 tacgtatttg tggaattgct gggccatgtg gtaatagatg ggtaactgta taagaaactg 300
57 ccataccact ttacaaattg gctgccacat tttttgcatt cctaccagca atatcagaca 360
59 ttcctatttt ttccatattc ttgccagtgt taagacttat catatgtcct ttttaacttta 420
61 tctgctctag gtgagtgtgt atggtttctc attgtggttt taacttgcac ttctttgatg 480
63 actagatttg ttgctatct tttcatgttc atctaagcga cttattacat atattttatg 540
65 aactattttg caaattcaat gattaattcc agagactttt tcagaattcc ctagtgtttt 600
67 ctacatatat aatgaagttg gtgacaaaga aagactttca tttcttcctt tcttatccat 660

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Input Set : F:\ARS-125-SEQ LIST.txt

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73 tacaggcatg agccaccatg cctggctcct gttgcactgg ttaggatgac tgttaggtgt 840
75 ttaaacaaga atg atg aga gct cac atg ttt gtt tac aag gaa ctt aaa 889
76 Met Met Arg Ala His Met Phe Val Tyr Lys Glu Leu Lys
77 1 5 10
79 caa att tac aag aaa aaa acc cat ccc cat caa aaa gtg ggc aaa gga 937
80 Gln Ile Tyr Lys Lys Lys Thr His Pro His Gln Lys Val Gly Lys Gly
81 15 20 25
83 tat aaa cag aca ctt ctc aga gga aga cat tta cgt ggc caa gaa aca 985
84 Tyr Lys Gln Thr Leu Arg Gly Arg His Leu Arg Gly Gln Glu Thr
85 30 35 40 45
87 tat gaa aaa aag ctc aca cac gta tat gaa ac gtgactgttt ataactctat 1037
88 Tyr Glu Lys Lys Leu Thr His Val Tyr Glu Thr
89 50 55
91 ccaaaaaaag a act gat ttc aag caa cag cag tat tac ttc cat tca ata 1086
92 Thr Asp Phe Lys Gln Gln Gln Tyr Tyr Phe His Ser Ile
93 60 65
95 ctt gga cct gca aac atc aaa aaa gcc act gga gaa act gaa cga ctc 1134
96 Leu Gly Pro Ala Asn Ile Lys Lys Ala Thr Gly Glu Thr Glu Arg Leu
97 70 75 80 85
99 tct gaa agc ctt aaa cta aga tat gaa gaa gtt gaa atc tgg aaa aaa 1182
100 Ser Glu Ser Leu Lys Leu Arg Tyr Glu Glu Val Glu Ile Trp Lys Lys
101 90 95 100
103 ctt gag gaa aag gac agg cag ggg gaa gca cag tgg cta caa caa aaa 1230
104 Leu Glu Glu Lys Asp Arg Gln Gly Glu Ala Gln Trp Leu Gln Gln Lys
105 105 110 115
107 agg cag gaa aca gga aga gag gat ggc agc atg ttg gct aaa ggt tct 1278
108 Arg Gln Glu Thr Gly Arg Glu Asp Gly Ser Met Leu Ala Lys Gly Ser
109 120 125 130
111 ttg gag att gta ttg gat tcc aaa gac aaa acc caa aag agc aat ggt 1326
112 Leu Glu Ile Val Leu Asp Ser Lys Asp Lys Thr Gln Lys Ser Asn Gly
113 135 140 145
115 gaa aag aat gaa aaa tgt gag acc aaa gag aaa gga gca atc aca gca 1374
116 Glu Lys Asn Glu Lys Cys Glu Thr Lys Glu Lys Gly Ala Ile Thr Ala
117 150 155 160 165
119 aag gaa cta tac aca atg atg atg gat aaa aac atc agc ttg att ata 1422
120 Lys Glu Leu Tyr Thr Met Met Met Asp Lys Asn Ile Ser Leu Ile Ile
121 170 175 180
123 atg gat gct caa aga atg cag gat tat cag gat tcc tgt att tta cat 1470
124 Met Asp Ala Gln Arg Met Gln Asp Tyr Gln Asp Ser Cys Ile Leu His
125 185 190 195
127 tct ctc agt gtt cct gaa aaa gcc atc agt cca gga gtc act gct agc 1518
128 Ser Leu Ser Val Pro Glu Lys Ala Ile Ser Pro Gly Val Thr Ala Ser
129 200 205 210
131 tgg att gaa gca cac ctc cca gat gat tct ata gat aca tgg aag aag 1566
132 Trp Ile Glu Ala His Leu Pro Asp Asp Ser Ile Asp Thr Trp Lys Lys
133 215 220 225
135 agg ggg aat gtg gag tat atg gta ctt ctt gac tgg ttt agt tct gca 1614

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137 230          235          240          245
139 aaa gat tta cag att gga aca aca ctc tgg cat ctg aaa gat gca ctt 1662
140 Lys Asp Leu Gln Ile Gly Thr Thr Leu Trp His Leu Lys Asp Ala Leu
141          250          255          260
143 ttc aag tgg gaa a gtaaaactgt cctgtgcaat gggccttggg cctttgggttt tag 1718
144 Phe Lys Trp Glu
145          265
147 ag gga ggc tat aaa aac tgg ttc ctt tgc tat tcc cag tat aca aca 1765
148 Lys Gly Gly Tyr Lys Asn Trp Phe Leu Cys Tyr Ser Gln Tyr Thr Thr
149          270          275          280
151 aat gct aag gtc act cca ccc cca caa cac cag aat gaa gag ttg tct 1813
152 Asn Ala Lys Val Thr Pro Pro Pro Gln His Gln Asn Glu Glu Leu Ser
153          285          290          295
155 atc tca ttg gat ttt act tat ccc tca ttg gaa gaa tca att cct tct 1861
156 Ile Ser Leu Asp Phe Thr Tyr Pro Ser Leu Glu Glu Ser Ile Pro Ser
157          300          305          310
159 aaa cct gct gcc gag atg cca cct cca cct ata aaa gtg gat gaa gac 1909
160 Lys Pro Ala Ala Glu Met Pro Pro Pro Pro Ile Lys Val Asp Glu Asp
161          315          320          325
163 ata gaa ttg ata agt gat caa ata agt gat aat gat caa aat gag agg 1957
164 Ile Glu Leu Ile Ser Asp Gln Ile Ser Asp Asn Asp Gln Asn Glu Arg
165 330          335          340          345
167 aca gga cca ctg aat ata tca att cca gtt gaa tca gtt gct gct tct 2005
168 Thr Gly Pro Leu Asn Ile Ser Ile Pro Val Glu Ser Val Ala Ala Ser
169          350          355          360
171 aaa tct gat gtt tca ccc atc att cag cca gtg cct agc ata aag aat 2053
172 Lys Ser Asp Val Ser Pro Ile Ile Gln Pro Val Pro Ser Ile Lys Asn
173          365          370          375
175 gtt cca cag att gat cat act aaa aaa ctg gca gtc aaa ttg cct gaa 2101
176 Val Pro Gln Ile Asp His Thr Lys Lys Leu Ala Val Lys Leu Pro Glu
177          380          385          390
179 gag cat ata atc aaa tct gaa agt aca aat cat gag caa cag tct cct 2149
180 Glu His Ile Ile Lys Ser Glu Ser Thr Asn His Glu Gln Gln Ser Pro
181          395          400          405
183 cag aat gaa aaa gtt att cct gat tgt tcc acc aag cca gta gtt tcc 2197
184 Gln Asn Glu Lys Val Ile Pro Asp Cys Ser Thr Lys Pro Val Val Ser
185 410          415          420          425
187 tct cca act ctc atg tta aca gat gaa gaa aag gct cat att cat gca 2245
188 Ser Pro Thr Leu Met Leu Thr Asp Glu Glu Lys Ala His Ile His Ala
189          430          435          440
191 gaa act gct ctt cta atg gag aaa aac aaa caa gaa aaa gaa ctt cag 2293
192 Glu Thr Ala Leu Leu Met Glu Lys Asn Lys Gln Glu Lys Glu Leu Gln
193          445          450          455
195 gaa aga cag caa ggg aaa cag aaa gaa act gag gag gga aga aca cga 2341
196 Glu Arg Gln Gln Gly Lys Gln Lys Glu Thr Glu Glu Gly Arg Thr Arg
197          460          465          470
199 gca aaa agc caa aaa gaa aca aga agc tga agaaaatgaa attacacaga 2391
200 Ala Lys Ser Gln Lys Glu Thr Arg Ser

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207	gtgatcatga	aacctctggt	gccgagaagt	ctgtagagga	cagggggaga	agatgttcaa	2571
209	ccccagaagt	acagaaaaag	tcaacaagag	atgtgtccca	tacatctgcg	acaggggatt	2631
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227	agatttggaa	actcaatcct	gtttttggag	gttctggacc	agctcttact	ggacttcgta	3171
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231	tggctgatta	tttcaaccga	aactgttatc	aggatgatat	taacaagtca	aatttgttag	3291
233	gggcataaag	gtgaagtggc	agaagaatth	ggtataatca	tgaaagcccc	gtggacagga	3351
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357 agaaaatgtg gcacatatac accacagaat accatgcagc cataaaaaag aatgagatca 7071
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376 <223> OTHER INFORMATION:

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/570,121

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Input Set : F:\ARS-125-SEQ LIST.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

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Seq#:31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,57,58,59

Seq#:60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,76,77,78,79

VERIFICATION SUMMARY

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Input Set : F:\ARS-125-SEQ LIST.txt

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L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:35 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:27
L:46 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:38
L:384 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:376
L:1523 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:52,Line#:1516
L:1871 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:55,Line#:1869